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# Making the microbiome public: Participatory experiments with DNA sequencing in domestic kitchens

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Recent rapid increases in the capability and affordability of DNA sequencing have enabled scientists to map the microbiome and to identify its associations with a range of health conditions. Concerns are growing that missing microbes might be behind the current rise in inflammatory disease. Microbial absence and dysbiosis have been linked to a range of hygiene practices, fuelling popular anxiety and confusion about being both too clean and the risk of superbugs. A growing number of microbiology projects allow some publics to engage with DNA sequencing, and enable DIY experiments in microbiome management. Advocates promote this as the democratisation of sequencing. This paper outlines a new methodology for making the microbiome public, and explores the potential of thinking with microbes for social science research. It reports on an interdisciplinary research project, in which a small number of households in Oxford designed and conducted repeated experiments on their kitchen microbiome. These experiments explored the composition of the microbiome and the effects of different hygiene practices. The analysis identifies two challenges of public microbiome research: the mismatch between a vernacular species ontology and the ecological understanding of the microbiome, and the difficulties posed by scientific uncertainty. The reported methodology was able to engage publics in the design and interpretation of experiments, and to work with the surprises generated by open research. Thinking with microbes as ecologies revealed the tensions between an antibiotic and a probiotic approach to domestic hygiene. Public microbiome research needs new metaphors and visualisation tools, and an awareness of the political economic and epistemic barriers that will configure the promised democratisation of sequencing. The conclusion calls for further interdisciplinary and participatory microbiome research to guide the emergence of this new technology.

## KEYWORDS

DNA sequencing, home, hygiene, microbiome, public science, science and technology studies

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# 1 | THE MICROBIOME, DYSBIOSIS AND CITIZEN SCIENCE

The Human Genome Project drove significant reductions in the cost and speed of DNA sequencing. Since its completion in 2003, scientists have turned their attention to microbial life forms, principally bacteria. High-throughput technology now facilitates metagenomics – the sequencing of the genomes of large numbers of microbial taxa in samples gathered directly from the environment, rather than those from single taxa isolated from laboratory cultures. Metagenomics has helped map a vast diversity of previously invisible microbial life. In so doing it created the microbiome, a new epistemic object variously defined as either the collective genomes of the microbes that live in an environment, or the combined ecology of the microbes themselves (Turnbaugh et al., 2007).

This research is most developed in the context of the human microbiome and its relationships with health and hygiene, focusing on the role of microbes in key bodily processes like metabolism, immunity and cognition (Lloyd-Price et al., 2017). Medical researchers warn of a global imbalance in microbial flora – or “dysbiosis” (Levy et al., 2017) – linked to “missing microbes” (Blaser, 2014). They argue that these cause “epidemics of absence” (Velasquez-Manoff, 2012), manifest in the recent rise in the West of allergic, auto-immune and inflammatory diseases. This thinking flags the role of beneficial microbes, but more profoundly, it shifts the clinical focus from microbial species to microbial ecologies, emphasising the importance of microbial diversity and of the functional roles played by microbial communities.

Microbiologists and immunologists have linked microbial dysbiosis to a wide range of health, hygiene and lifestyle practices. Their investigations pick up on, and are arguably co-produced alongside, concerns with the risks posed by excessively antibiotic ways of managing microbial life (Lorimer, 2018). A “hygiene hypothesis” explaining increases in allergy was proposed in the late 1980s (Strachan, 1989). It has subsequently been refined in light of the microbiome to a “biome depletion hypothesis” (Parker, 2014). This differentiates beneficial “old friend” microbes, with which humans co-evolved, from undesirable “crowd infections” associated with agricultural, and then modern life (Rook, 2009). This thinking profoundly challenges the modern germ theory of disease and the antibiotic approaches to public health it has informed, what Tomes (1999) has called the “gospel of germs.” Instead, it identifies the need for “targeted hygiene” (Bloomfield et al., 2016) that can better differentiate between desirable and undesirable microbial exposures and forms of microbial management. Prominent microbiome scientists have begun advocating probiotic approaches to healthcare, diet and hygiene in books with titles like *Dirt is good* (Gilbert & Knight, 2017) or *Let them eat dirt* (Finlay & Arrieta, 2016).

In the UK (which is the focus of this study) and elsewhere, these ideas have fuelled public anxieties about how best to live with microbes. In popularising the hygiene hypothesis, media coverage has amplified the dangers of antibiotic excess, while simultaneously reminding readers of the dangers of microbial pathogens, such as particular strains of *Campylobacter* and *Salmonella*, and of antibiotic-resistant super-bugs. Mixed messages and confusion are ubiquitous (Bloomfield, 2017). In response, publics have been engaging in DIY microbial experiments, involving interventions as diverse as fermenting food, probiotic health and hygiene products, exposure to domestic animals, “messy play,” faecal microbiota transplants and “seeding” to replicate vaginal microbial exposure in babies born by Caesarean section (see Lorimer, 2017; Spackman, 2018; Wolf-Meyer, 2017).

This scientific and popular interest in microbes has fuelled excitement about the potential of metagenomics for researching and diagnosing dysbiosis, and for informing microbiome management in the body and in the built environment (Maxmen, 2017; Microbiology Society, 2017; National Academies of Sciences, Engineering, and Medicine, 2017). These interests are driving efforts to engage publics with the microbiome. These include traditional models of scientific research (like the Human Microbiome Project) in which publics are enrolled by clinicians to provide representative samples of microbial diversity. They encompass studies in which publics participate as donors and patients in clinical trials of microbial therapeutics (for example, of faecal microbiota transplant). But microbiome research is also being facilitated by a heterogeneous collection of citizen science, crowd-funded and DIY projects (cf. Hogarth & Saukko, 2017 on the human genome). In these efforts to make the microbiome public (after Latour & Weibel, 2005), publics are involved in sourcing microbial samples, funding personalised sequencing and interpreting their results, and engaging in their own experiments in personal microbiome management.

Proponents of this public microbiome science – like those involved with the “citizen science” project uBiome – speak of the “democratisation” of microbiome research (Richman, 2013). They speculate as to its radical potential to recalibrate how people think about their health, their relationships with others and the environment. There is a lot of hype in this “microbiomania” (Helmreich, 2015; Paxson & Helmreich, 2014; Slashinski et al., 2012), but it is clear that the technologies of metagenomics and the science of the microbiome are beginning to spill out from the laboratory to touch down in the bodies and homes of wider publics. This spillover is only likely to increase with the ongoing miniaturisation and simplification of sequencing machines and their decreasing cost (Check Hayden, 2015).

While these ideals of democratisation and citizenship are prominent in the narratives of those involved in taking metagenomics out of the lab, in practice most of these projects are premised on a rather modest redistribution of political agency, and a rather narrow appreciation of the epistemic diversity associated with public understandings of microbes (Shamarina et al., 2017). While publics may be involved in the scientific process as microbial gatherers or data-recipients, they rarely get to shape the agenda of the research projects they are involved in. Nor is much attention given to how these technologies interface with vernacular hopes and anxieties about dysbiosis and the promises of microbial therapeutics. The emergence, conduct and translation of microbiome science raises a wide range of ethical, legal and social issues, some of which have been considered elsewhere (Benezra, 2016; Nading, 2016; Rhodes et al., 2013; Stallins et al., 2018).

This paper engages with a specific subset of the social dimensions of the microbiome and of metagenomics. The primary aim of this research was to redefine the project of democratising metagenomics, by developing a methodology that enables a specific public to explore and experiment with microbiome sequencing technologies in their everyday lives.<sup>1</sup> We wanted to engage our public with the process of *doing* microbiology, and with discussing and deliberating the generated data. Making microbiome sequencing technologies public in this way offers an important testbed for examining the social possibilities, risks and challenges that will be associated with the future proliferation of microbiome-sensing devices, and the new forms of microbial citizenship they might engender. Our secondary aim was to explore the potential of participatory microbiome science as a tool for social science research. We examine how thinking with the microbial ecologies made visible in our public experiments offers new insights into human–microbial relations. This study focuses on understandings and practices of domestic kitchen hygiene in the UK, as they are shaped by the hygiene hypothesis, and popular concerns and confusions about the best way of living with microbes. We hope, however, that this methodology might be applied to a great diversity of human–microbial relations. We outline the methodology in detail below, but before doing so we will briefly position our approach in relation to existing literatures on public science.

## 2 | OPEN AND PARTICIPATORY SCIENCE WITH EMERGENT PUBLICS

In conceiving our methodology, we were influenced by three overlapping literatures within the burgeoning research and practice on public engagement with science and technology. The first is a long-standing interest in science and technology studies and its focus on opening up laboratory spaces and the black boxes of scientific technologies, like those involved with DNA sequencing (Levin, 2014; Mackenzie, 2003; Rabinow, 1996a, 1996b). There is a long history of ethnographic work in which social scientists shadow laboratory scientists to better understand the social norms, material assemblages and political interests that come to frame the production, circulation and governance of science (Latour & Woolgar, 1979). The emphasis here is on following the things of science into and out of private and proprietorial spaces, to trace the process of political and epistemic enclosure and exclusion. This openness has been extended more recently from social scientists to members of the public, with the rise of what has become known as the “co-production of knowledge model” (Chilvers & Kearnes, 2015; Whatmore, 2009). Here collectives of researchers, with varying forms of expertise, work together to generate knowledge. These collaborations seek to break down the divides between scientific and lay knowledge and between citizens and their political representatives (Callon et al., 2009), with varying degrees of success (Wilsdon & Willis, 2004). The normative arc in these accounts is towards “opening up” (Stirling, 2008) controversial scientific and technological developments. When done well, participation and co-production are seen to deliver more accurate, legitimate, democratic and critical forms of science and, it is hoped, policy (for a compelling microbiological example, see Waterton & Tsouvalis, 2015).

Second, these literatures on public science suggest that it is unhelpful to view the public of science as a singular or pre-existing thing. Instead, publics are heterogeneous and contingent. That is, they are made up of people with a diversity of experiences and knowledges. These publics might emerge and cohere through shared practices (Eden & Bear, 2012), or be “sparked” into being by emerging issues or events (Marres, 2005). This work presents knowledge controversies as the generative events through which sciences’ publics are made (Whatmore, 2009). Here confusion and controversy are not necessarily failures but can be generative and are vital for the political functioning of technical democracies (Callon et al., 2009). Work in this vein has attended to the affirmative roles of popular scientific technologies in provoking publics into being (Harris et al., 2013; Marres, 2012), while others have mobilised scientific technologies as the fulcrums for DIY or citizen science and for collaborative hacking projects (da Costa & Philip, 2008; Gabrys, 2016). The consistent aim of these endeavours is to democratise scientific technologies and the data they produce, making them accessible, accountable and affordable to those they might benefit.

Third, we take inspiration from a parallel tradition of participatory action research, more commonly associated in geography with community-based development projects (Kindon et al., 2007). In its strictest application, this approach starts

from soliciting the interests of an assembled public, which then come to form the agenda of the research project. Our project did not take our publics' interests this far upstream (Wilsdon & Willis, 2004), but we were drawn first to the emphasis in this approach on recursive and longitudinal modes of deliberation. Proponents advocate structuring group work around a "deliberation-action-reflection cycle" (Kindon et al., 2007), in which researchers and publics work together to build trust, confidence and expertise through repeated facilitated meetings. We develop this approach in the account that follows. Furthermore, participatory action research attends to the political and methodological potential of visual imagery, including simple drawings and maps, alongside the production of moving imagery, and the development of more complex and abstract visualisation tools (Crampton, 2009; Kindon, 2003; White, 2003). Visualising the microbiome proved to be an important, yet challenging, component of our methodology.

In drawing these approaches together, our approach borrowed most extensively from the apprenticeship model of knowledge co-production, developed by Sarah Whatmore and her co-researchers in the context of flood management in northern England (Whatmore & Landstrom, 2011). This approach enables affected publics, and various social and natural scientists, to develop new, shared understandings of key issues. In the case of flood management, lay and scientific experts jointly learnt to use and develop scientific tools and methods, primarily hydrological models. Whatmore et al.'s work has demonstrated how shared public-scientific endeavour allows for effective engagement because publics are given the ability to frame and re-frame the questions asked through science, rather than being limited to interpreting the implications of scientific research after the fact. As we detail below, through becoming apprentices in scientific practices, we (social and natural scientists) found our way collaboratively into the initially black-boxed science of metagenomics. We were then led by our participants into a second apprenticeship in which we together become a specialised public (Eden & Bear, 2012), distinguished by its practical and knowledge competencies around a particular issue (domestic hygiene in light of the microbiome) and its scientific technologies (metagenomics).

In this apprenticeship we worked collaboratively through the confusion generated by the microbiome to refine our methodology and to identify the priority questions for scientific and social scientific research on domestic hygiene. We should be clear at this point that our aim was not to generate a solution to the current confusion about hygiene in light of the microbiome. We did not set out to build consensus, or to arrive at a decision to be applied in public policy. Instead, our engagement was, in an important and explicit sense, about generating questions and identifying challenges. This mode of agenda-creation stands in stark contrast to the more familiar expert reviews that are being used to shape microbiome research priorities (e.g., Microbiology Society, 2017).

### 3 | A PARTICIPATORY METHODOLOGY FOR MICROBIOME RESEARCH

This was an interdisciplinary research project conducted by a team of six human and physical geographers from the University of Oxford in 2016–2017. The project was funded by the UK Economic and Social Research Council in partnership with the Food Standards Agency (FSA). In embarking on the project, we did not recruit an existing, mobilised public or sample a representative subset of a population at large. Instead we assembled a self-selecting group of participants with a curiosity about microbes and their implications for everyday life. For practical reasons, we focused on a suburban area of Oxford with an accessible community centre to host the group meetings. We posted adverts on relevant social media, in the community centre and newsletter, and in local shops. The adverts were framed to pique curiosity about what lives in the kitchen: the project was entitled "Good Germs, Bad Germs."<sup>2</sup>

In designing our recruitment material, we sought to generate applications from multigenerational and multispecies households. Conversations with our FSA partners, and a review of the microbiological, public health and popular literatures, drew our attention to the importance of generational differences in hygiene practices. It also suggested that children and animals generate interesting microbiomes, and that they have been implicated in concerns about missing microbes and beneficial exposure (Blaser, 2014; von Mutius & Vercelli, 2010; Wills et al., 2013). We offered a £150 shopping voucher as compensation for our participants' time and effort. After asking respondents to complete a short questionnaire,<sup>3</sup> we recruited 14 households. In total, the project involved 21 adults (13/8, F/M), 14 children, nine dogs, three cats and an assortment of other domestic animals. Our human participants were mostly White British with above average incomes. They had a range of professional and personal microbiological and hygiene expertise, from contexts including catering, cleaning, clinical work and dietary advice. The project received ethical approval through the University, and all participant data were anonymised.

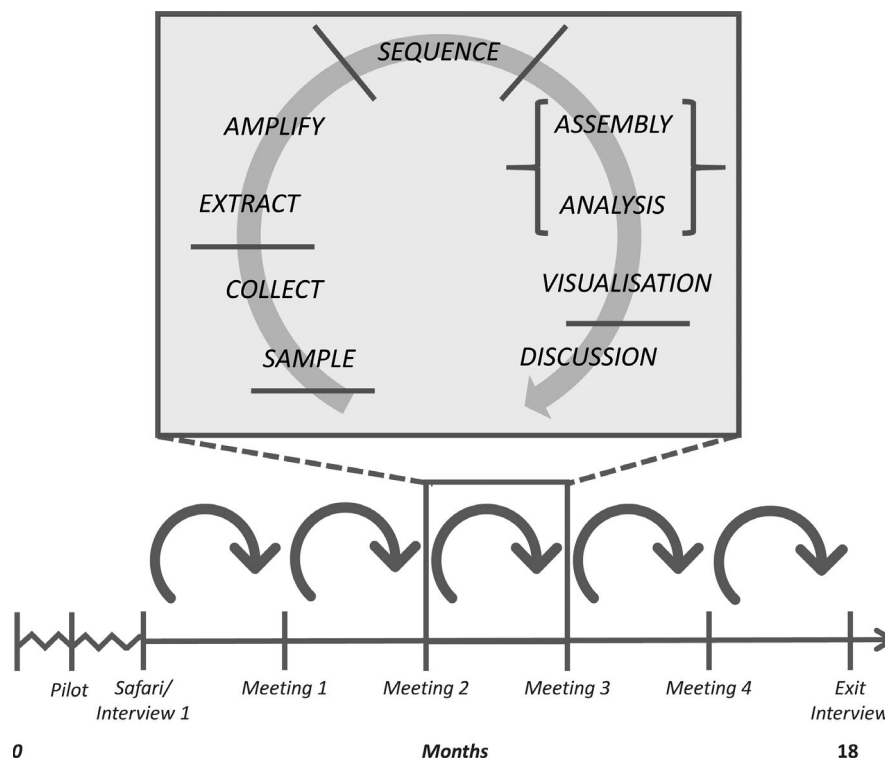
A timeline of our methodology is presented in Figure 1. Two of the human geographers first visited each household and conducted an entry interview. They asked participants about their knowledge and perceptions of microbes, and how they



felt these informed their cleaning and cooking practices. Questions explored their knowledge of the hygiene hypothesis and what, if any, concerns they had about being too clean. At the end of the interview we proposed the first group experiment, which we had designed in advance. This was a kitchen safari, for which all participants were to sample five common sites (a work surface, sink, chopping board, cupboard door handles and floor), and a sixth of their choosing. The five sites were selected so that we could compare with existing research on the domestic microbiome (Dunn et al., 2013; Flores et al., 2013). Giving participants a choice of the final site required them to begin the process of thinking with microbes. We left open where they should sample but explained that we were not able to handle samples of human or animal material (for which we did not have ethical approval). We gave them their sampling kits and explained how they were to be used, stored and collected (Figure 2).

The households' metagenomics apprenticeships then took place through a series of six, two-hour group meetings, conducted over an 18-month period in the local community centre. We began the first group meeting with a simple icebreaker exercise in which we asked them to colour in a plan to show where they thought the greatest diversity of microbes would be found in their kitchens. We introduced the science of genomics and the laboratory techniques of DNA sequencing. We used YouTube videos and photographs of our laboratory work (see below) to help our participants understand the tools they were going to use, and to get them thinking about the experiments they might want to carry out. We then gave each household a personalised data pack, containing the visualised results of their own safari (Figure 3) and a comparison with the aggregated results from the other households. We discussed the differences between the expectations revealed in the colouring exercise and the visualised results, and asked them to explain their choice of site for the sixth swab.

Towards the end of the meeting, we solicited ideas for the second group experiment. After it finished, we built an online poll that listed all of the options suggested by the participants and encouraged households to vote by email on which three they would prefer. We drew up instructions for the most popular experiment and delivered the sampling kits. We repeated and refined this process over subsequent rounds of group meetings and experiments (see Table 1). At each meeting we discussed the results of the previous experiment and explored their implications for our participants' perceptions and practices of hygiene; we also worked on developing the best means of visualising the results. We invited a scientist from the FSA to join our discussions at one meeting. All households conducted the first four experiments, but we let them each design and carry out their own personalised final experiment. We discussed their experience of participating in the project at an exit interview, where we also returned to the questions about hygiene that we discussed in the entry interview. We asked for feedback on the project methodology.



**FIGURE 1** A timeline of the participatory methodology showing the stages of the metagenomics workflow.

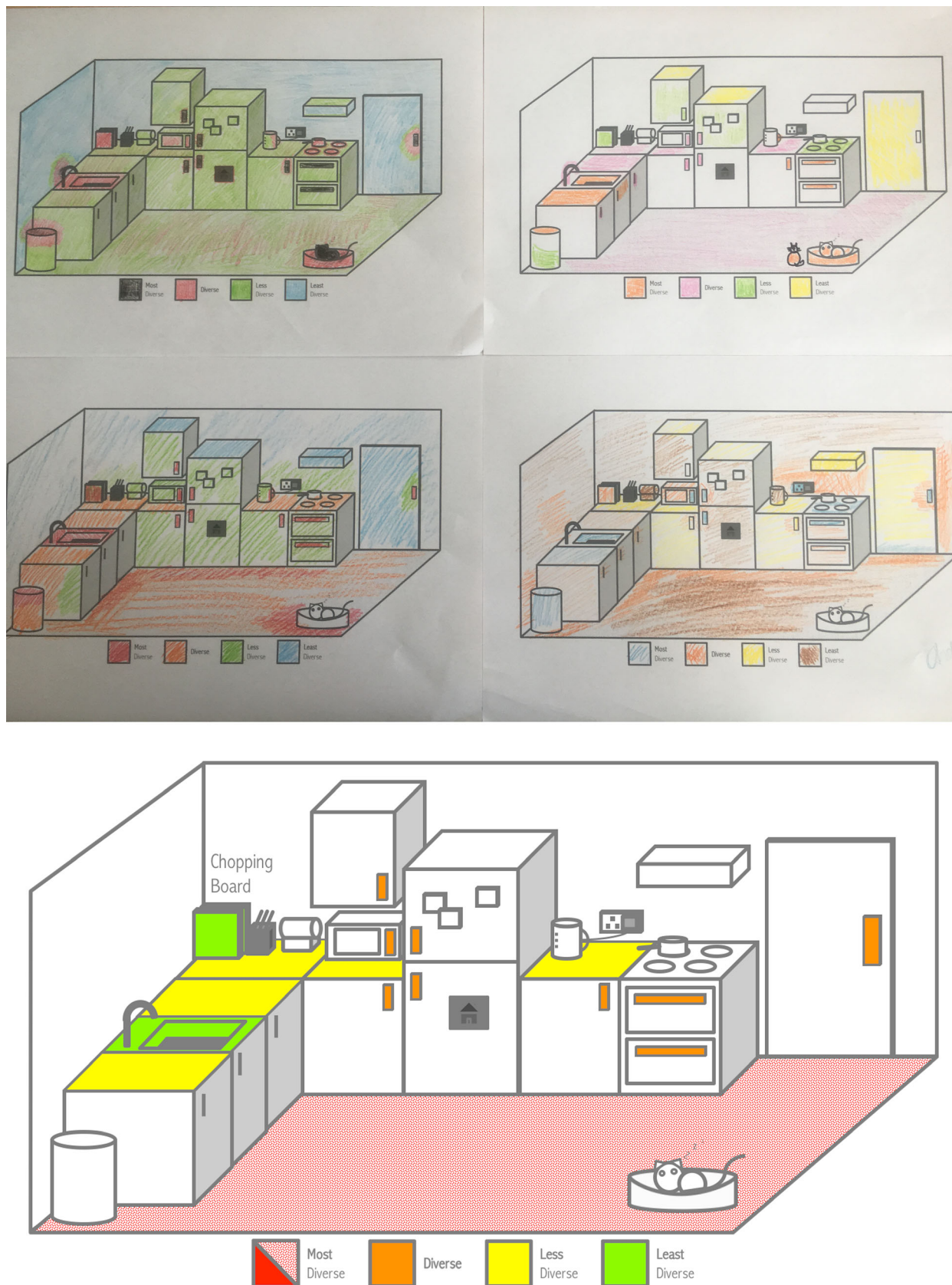


**FIGURE 2** The microbiome sampling and collection kit. [Colour figure can be viewed at [wileyonlinelibrary.com](http://wileyonlinelibrary.com)]

Over the course of the group meetings we aimed to progressively democratise our model of microbiome research, moving away from the more top-down version of citizen science seen in the safari – in which citizens were enrolled to collect data to answer a question pre-established by scientists – towards a version of “research in the wild” (Callon et al., 2009), in which the focus of the research was driven by the interests of participating publics. Participants were encouraged to form their own hypotheses as to what shaped their kitchen microbiome and to design corresponding experiments. This recursive microbiological apprenticeship (outlined in Figure 1) aimed to develop a “collective learning cycle,” akin to the deliberation-action-reflection cycle of participatory action research. Here we were inspired by the pedagogical theories of Jerome Bruner (1960). His notion of the “spiral curriculum,” drawing on constructivist approaches to cognition, involves re-visiting a topic multiple times over the course of a child’s education. Using this process, learning works through facilitating curiosity and discovery with each visit, but with the conceptual complexity increasing with each return. In our case (and working with adults), the aim was to use the cycle of repeated experiments and deliberations to facilitate the group’s (ongoing, unfinished) apprenticeship in understanding both the methodological possibilities of the sequencing methodology and the complexities of microbial ecology. Our own and our participant group’s understandings (and sometimes, sense of bewilderment) grew with each cycle.

As might be anticipated, metagenomic sequencing is not a simple process. As a totality of genetic material, the microbiome cannot be seen *in vivo* down a microscope, nor can it be cultured *in vitro* in laboratory media. Instead a microbiome is created through a technoscientific “workflow.” This term is used by microbiologists to describe the steps through which environmental samples – like those swabbed onto a cotton bud in our kitchen safari and in the participatory experiments – are processed, sequenced, assembled, analysed and visualised (Figure 1). In a very real sense, the workflow makes the microbiome emerge, and there is some concern among scientists about how different workflows might bring different microbiomes into being (Thomas et al., 2012).





**FIGURE 3** Expected and actual microbial diversity on the surfaces of all the kitchens sampled. This image was inspired by Flores et al. (2013).



**TABLE 1** Details of the participatory experiments. Each experiment involved one of the cycles illustrated in Figure 1. The sequence of the experiments followed the numbering of the group meetings shown in this timeline.

Experiment	Research question	Sites sampled
Kitchen safari	What lives in your kitchen?	Work surface, sink, chopping board, cupboard door handles, floor, and one other
Cleaning products	What difference do cleaning products make?	Cloth and work surface before and after using two different products
Chopping board	How is a new chopping board colonised?	Chopping board on day 0, 1, 2, 4, 7, 14
Fridge ecology	What is microbiome of the fridge?	Composite of fridge surfaces, and four food items in fridge
Personal choice	Where do my pet's microbes show up? ( $n = 6$ )	Animal or animal bed, various domestic surfaces
	What is the effect of the Christmas tree on the domestic microbiome?	The tree, and a picture rail before delivery, and in days 1, 2, 7 and 14
	What is the difference between organic and conventional vegetables?	The surface of an organic and a non-organic carrot, kiwi and leek
	What is the difference in the domestic microbiome between term time and holiday?	Door handles, cupboard handles, and light switches before and during the holiday

No member of the project team was a bona fide (i.e., learned, certified, disciplined) expert in metagenomics, though one of us had sufficient training to undertake the necessary laboratory preparations. As such, all of the university researchers initially embarked on an extensive metagenomics apprenticeship to understand the rudiments of the science so that we could design and pilot our workflow. We read the key literature, spoke with other researchers working on the domestic microbiome,<sup>4</sup> and did a pilot project sampling our kitchens and interviewing each other on our cleaning practices. To map and open up the private spaces of the laboratory, a postdoctoral researcher (a social scientist by training) shadowed the project biologist and collected visual and ethnographic accounts of his experience. While participating in this metagenomic apprenticeship, he reflected constantly on the ways in which technoscientific spaces, relations and equipment were shaping our attempts to craft a more participatory practice. He attended in particular to the barriers to public understandings of and engagement with the microbiome encountered during this apprenticeship.

Our workflow came to be built around a technique called “16S ribosomal RNA sequencing,” which is commonly used in microbiology for identifying the different types of bacteria found in an environmental sample. Pioneered by the microbiologist Carl Woese, it works by isolating all the examples of a specific DNA sequence (the 16S rRNA gene) from a sample of nucleic material. While all bacteria have this gene, it contains sections that are variable between different types (species being a tricky concept when it comes to bacteria), allowing them to be statistically identified by comparing the 16S sequences against a known library. Our budget limited us to five sequencing runs (each of 96 samples) for the entire project.

As with much microbiological science, the technique involved a long series of steps and processes, which had to be followed and replicated according to strict protocols (outlined in broad terms in Figure 1). These took place in the secure and private spaces of a laboratory in Reading, to which we were given access after undergoing basic safety training. After bringing our samples to the laboratory, they had to be processed and documented, transferred into pre-labelled 1.5-ml Eppendorf tubes, and put through multiple cycles of heating and cooling, centrifuging and vortexing, with various buffer solutions added at key points along the way. These steps allowed us to extract and copy the key sections of genetic material necessary for identifying bacteria from the vast quantities found on the end of a cotton bud that had been repeatedly rubbed on a kitchen surface.

The spatial privacy enacted by the formality of the laboratory was mirrored by the private (or proprietary) character of many of the materials we used as the workflow progressed. For example, the various chemicals (enzymes, buffer solutions) used to instigate and control our DNA extraction and amplification processes were not assembled from stock ingredients in the laboratory. Instead they were purchased in a variety of commodified kits (in this case from the company Sigma-Aldrich). Each kit is proprietary, expensive and doesn't usually work well if used with another company's reagents or kits. It is hard or impossible to replicate kit contents: recipes are IP-protected and not usually made public – an important safeguard for corporations selling to a scientific culture in which biohacking and DIY are common practices. In the final laboratory stage of the workflow, we sent our prepared samples to the Wellcome Trust Centre for Human Genetics in Oxford for sequencing. We were given a tour of this facility, but were not involved in the actual sequencing. The machines

required are expensive and require specialist training and constant throughput to justify investment. Our samples joined the queue.

Back in our departmental offices, often after frustrating delays of several weeks or months for each cycle, we received datafiles from the sequencing machine and its operatives. In this stage of the workflow, questions of seclusion and openness were re-configured. Instead of proprietary chemicals and expensive machinery, here we relied on free, open-source bioinformatics software to reassemble our library and to visualise the microbiome. We initially used QIIME (Caporaso et al., 2010) and then UPARSE (Edgar, 2013). Processing this big data required significant computing capacity. The magnitude and the complexity of the data files, and the technological competencies necessary to process this information, enacted a form of epistemic exclusion. DIY microbiologists, quantified selfers (Lupton, 2016) and bio-hackers use these tools, but they proved challenging to deploy and make public. Nonetheless, this analysis generated a range of visual and graphical outputs that became the primary means through which we returned the data to our participants and structured our group discussions in the community centre.

## 4 | THE CHALLENGES OF PARTICIPATORY MICROBIOME RESEARCH

Before evaluating how our methodology delivered on its aims, we want to foreground two important challenges that we encountered in making use of the outputs of the laboratory work in our group meetings. The first relates to the popular power of a species ontology, the second with how to handle scientific uncertainties. We explain these challenges below, dwelling on what they imply for current and future efforts to make the microbiome public in the context of domestic hygiene.

### 4.1 | The species ontology

The data generated from each experiment was copious: a list of perhaps 100,000 potentially different 16S rRNA sequences from each of the 96 samples, with each sequence being comprised of a list of around 1,500 base pairs. To sort the data, anything with up to 15 base pairs (1%) difference was clumped together and treated as an “operational taxonomic unit” (an OTU), which is, in some ways, a proxy for a species of bacteria. This type of species ontology has proved valuable for driving public science in the macrobiome. Species (of birds, mammals, butterflies, etc.) configure the logics and metrics of wildlife monitoring, research and conservation. They have popular appeal. We had mobilised this ontology in the title of the project “Good Germs, Bad Germs,” in the framing of our first experiments as a kitchen “safari,” and by introducing our participants to some soft toy “giant microbes” in the opening meeting.<sup>5</sup>

From our interviews, we learnt that our households tended to understand microbial life in terms of individual pathogens. They were mostly familiar with the strains of bacteria that feature regularly in the media: *E. coli*, MRSA, campylobacter, etc. They were well acquainted with “the gospel of germs” as promoted in the advertising materials of domestic hygiene products (kills 99.9% of bacteria, etc.), as well as with the idea of probiotic dietary supplements, based on specific bacteria strains. When we first asked them how they would like their data presented, they requested pictures of individual microbes, biographies of what they did and quantified counts of their relative abundance before and after their designed interventions. Generating quantitative data on bacterial species or strain is fairly standard practice in microbiology for public health and swabbing for pathogens involves relatively simple and everyday science.

However, in this project we wanted to move away from this pre-microbiome ontology of microbial life based on visible and/or culturable strains, and the antibiotic orthodoxy of the germ theory of disease it informed. Our aim was to try and introduce the new ecological ontology of the microbiome and of dysbiosis, which is focused on microbial qualities: diversity, abundance and the functional roles performed by microbial ecologies. We wanted to explore the emerging public health messaging about microbiome dysfunction, and to dwell on its mismatch with longer-established and still commonplace antibiotic norms. We therefore needed to work with our participants to form new understandings around a new ecological object – the microbiome – and to encourage them in their considerations of the ubiquitous and commensal nature of much microbial life.

Sorting and visualising our microbiome data for discussion in the group meetings therefore posed significant challenges. The vast majority of our samples had extremely high levels of bacterial diversity. Representing this diversity at the familiar taxonomic level of species was problematic as the data generated through our workflow became less reliable the lower the taxonomic level we were working with. We were not convinced of its accuracy when it came to the species level. To present microbial diversity, we were compelled to use the higher-level taxonomic categories (like the phylum) that shape the

tools for visualising the microbiome that we drew from bioinformatics. Microbiologists are (at best) ambivalent about the utility of the species concept for assessing biological relationship (Bordenstein & Theis, 2015). Their scientific interest is often in evolutionary origins, ecological relationships and community dynamics. They tend to configure and visualise their data around higher taxonomic levels (see Figure 4).

We drew on these tools, but it fast became apparent that our participants were not used to thinking of bacteria in terms of evolved communities at the level of phyla. As one participant explained:

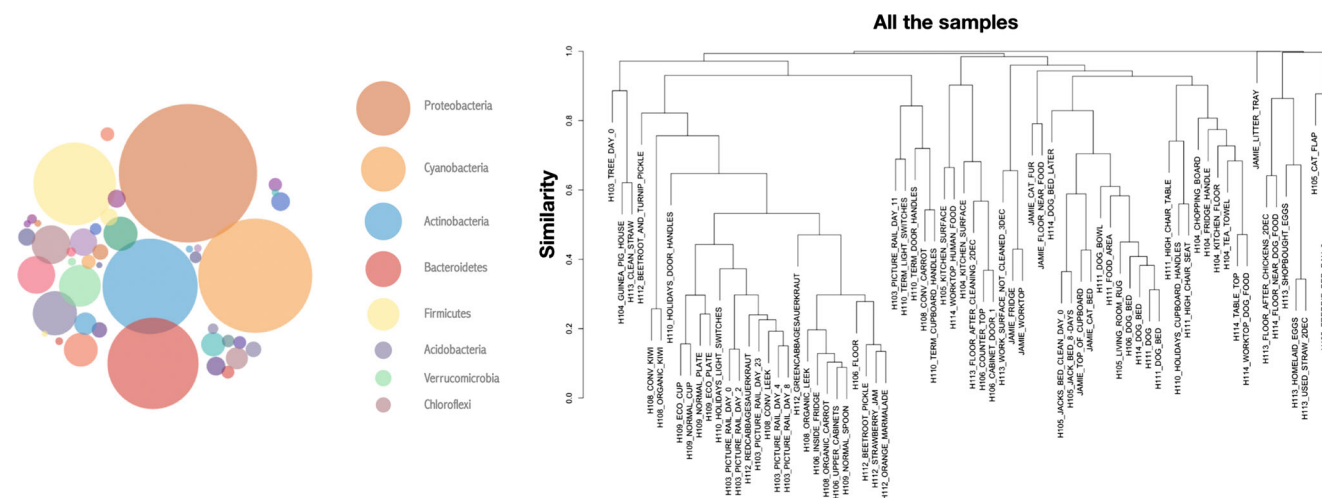
It was interesting to know the sheer scale of the microbial life but it also seemed quite abstract that some of names of things ... it's just sort of abstract words and families that don't-, it seems difficult to kind of connect to in some ways. (Household 111, Exit interview, July 2017)

There was an understandable desire to know what bacteria – or more specifically, what pathogenic bacteria – might have been present. In retrospect, we may not have helped ourselves by titling the project “Good Germs, Bad Germs.” But this situation identifies some of the challenges that face those using metagenomics as a tool for engaging publics with the microbiome. Our workflow was good at revealing classes of microbes, mapping abundance and diversity, tracing evolutionary relationships and identifying likely sources. It was less good at listing individual microbial species. As such, our workflow was based on an unintuitive ontology – or unfamiliar worldview – for making the microbiome public. As one participant put it:

Remember there was the blob one time when none of us could seem to understand it at all [laughter]. There was this kind of desperate long explanation of it and then at the end of it we all looked at each other and said, ‘Nah, I still don't get it.’ [laughter] (Exit Interview 104, July 2017)

We frequently experienced confusion and pushback. We found ourselves caught between explanation (educating our public in microbial ecology) and participatory deliberation (recognising the interests, needs and challenges our publics were identifying through their experiments). This situation exposed the limits posed to participation by a method (16S sequencing) that was not tailored to answer our participants' questions.

As the technologies of metagenomics continue to spill out of the laboratory, there will be a technical need for bioinformatic and visualisation platforms better attuned to the vernacular microbiologies of the publics they seek to engage. Such platforms are beginning to emerge in the online “dashboards” used by some personalised sequencing companies (like uBiome), which offer accessible and aesthetic graphics, and narrate the functional roles of different bacterial phyla. In retrospect, our project could have dedicated more resource to developing an equivalent platform for the microbiome of the built environment, but (as we explore below) the scientific evidence base for such a tool is still in its infancy.



## 4.2 | The challenge of scientific uncertainty

As our metagenomics apprenticeship developed through our collective learning cycle, it became clear that the group's learning was being strongly shaped and constrained by a series of scientific uncertainties relating to both the sequencing methodology and the underlying microbial ecology it sought to represent. As discussed above, the inability of our workflow to identify specific pathogenic strains of bacteria was a source of ongoing frustration among our participants. In addition, one of the quirks of swab sampling of the environment, when compared to more traditional culturing techniques, is that while it can identify what DNA is present on a swab, it cannot tell you if that DNA was from a living organism. Put plainly, our method couldn't distinguish between live and dead bacteria, which posed a real problem when interpreting the experiments. This was especially the case with the experiment on the effects of different cleaning products, which appeared to demonstrate abundant bacteria on a worktop in the aftermath of it being bleached.

The wider issue of scientific uncertainty with respect to the microbiome was more fundamental than these methodological quirks. Often our participants wanted information about the implications (predominantly relating to human health) of having microbial communities of differing kinds on their kitchen surfaces that neither we nor the experts we consulted were able to provide. As one participant put it:

I felt that—, to be honest, if there was a slight let down in the whole thing [laughter], it was the, you know, not finding dangerous germs on objects, you know. There was no CSI type sort of—, it became apparent quite quickly that this wasn't going to be, wow, you know, if I'd used that breadknife one more time, you know, that would have been the end. (Household 104, Exit interview, July 2017)

Given the current state of scientific knowledge about the microbiome of the built environment, we were unable to say what forms of microbial community ecology were better for humans. This gap relates in part to the relatively early stage of development of the science in this area. In our introduction to the current state of the science around the microbiome (at the first group meeting), we explained that it is becoming clear that there is no single, normal healthy microbiome of the human gut (Lloyd-Price et al., 2016, 2017) or of the domestic environment (National Academies of Sciences, Engineering, and Medicine, 2017). While it is possible to detect situations of extreme dysbiosis, in most cases the presence of specific bacteria might not indicate disease, and different bacteria can fulfil the same functional roles. Epidemiological evidence points to the salutary effects of microbial diversity, and certain probiotic dietary and lifestyle practices (Velasquez-Manoff, 2012), but these effects develop over the life course and their causal mechanisms remain unclear.

There was a generalised anxiety that we detected in some of our households about the effects of domestic hygiene on their health, and especially the health of their children. This was especially true of those who suffered from an allergy or autoimmune disease, and had become aware of the hygiene hypothesis. We learnt that several of our participants were part of pre-existing communities – or what social scientists have described as biosocial, or even microbiological collectives (Blackman, 2016; Rabinow, 1996a, 1996b) – united around particular disease conditions. During group discussions and in interviews they proposed a range of hypotheses as to what their conditions were caused by (e.g., air pollution, chemicals, indoor lifestyles, diet, etc.) and explained where they had sought this information. Several participants explained that they came to the study because they wanted to find out more about the science and to investigate these hypotheses. But their theories were hard to explore and illustrate through the types of small-sample, snapshot experiments that we trialled in this project. We had to explain how they would require experiments of longer duration and with larger sample sizes.

This situation made clear a general priority for research around the microbiome and its relationships with domestic hygiene that can best be described by the recurrent question – sometimes explicitly stated in group meetings and interviews, other times communicated in a glance, a facial tick or a shift in posture – “what should we do?” The question relates to our participants' desires for guidance as to the correct or safe ways of managing microbes in their kitchens. The strength of this desire was made clear in the choices of experiments made by the participants, with two of the four (on chopping boards and cleaning products) being directly related to safety concerns. Our participants were not shy in voicing their disappointment that at the end of the project they felt no better informed as to what was a good or bad germ, what a healthy domestic microbiome looked like, or how they ought to cook and clean. The implications of our experience for domestic microbiome research are clear. There is a need for research that can distinguish healthy microbial ecologies in domestic settings, not based simply on the presence/absence of pathogenic strains of bacteria (as at present), but on the types of bacterial communities that protect against or facilitate pathogenic states. There is also a need to identify the everyday cleaning and cooking practices likely to result in “eubiotic” rather than dysbiotic states.



## 5 | THE POTENTIAL OF PARTICIPATORY MICROBIOME RESEARCH

It was nice to be able to have that kind of democratic vote of what we—, what was interesting to us and what was—, what we all found, you know, had in common that we wanted to find out, which was nice. So, I think that that was a really good aspect of it, to kind of feel that we did have some control but it was—, as participants in general we had—, we decided what we were doing. (Household 111, exit interview, July 2017)

In this section, we consider our experience of conducting this project in relation to its two stated aims. We first evaluate how our methodology contributes to ongoing efforts to democratise metagenomics and microbiome research. We then explore what thinking with the microbiome offers as a mode of conducting social science research into domestic hygiene practices.

### 5.1 | Open participatory experiments with emergent publics

Our use of sequencing exposed some of the challenges of taking this nascent technology out of the laboratory. It taught us a great deal about the potential of this type of public and interdisciplinary research. There are three contributions to flag here. The first emerges from the metagenomic apprenticeship undertaken collaboratively by human and physical geographers. Here a project researcher with social science training shadowed and was trained by the project biologist as they prepared the biological samples and secured their sequencing. This laboratory ethnography helped open up the black box of metagenomics, to understand the political and epistemic challenges of making the microbiome public. By embedding social science in the design and conduct of our workflow, we were also able to make sure that the solicited concerns and interests of our public shaped the experimental protocol. This interdisciplinary approach enabled a novel mode of biogeography, in which the embedded social scientist acts to channel and champion the interests of the public participants deep within the secluded spaces of the laboratory in order to develop research tools with greater potential to spark publics into being.

For example, the kitchen visualisations that are shown in Figure 3 were informed by our initial interview data on the vernacular microbiological knowledge and expectations of our participants. We reached for a visual reference that would be familiar to our participants: in this case (of largely aspirational home-owners) a two-dimensional map akin to the Ikea kitchen planning tool. Our subsequent visualisations were refined through our (sometimes uncomfortable) discussions at the group meetings. The recursive structure of our participatory methodology enabled us to take our participants on their own metagenomics apprenticeship. We were able to first build the microbial literacy within our group, then to allow our participants to discuss their own interests in the domestic microbiome and to develop their own hypotheses. At the same time, they also educated us, bringing their diverse expertise from clinical, culinary and care settings to enhance the group learning about the microbiome and hygiene in the built environment.

Any social science methodology is performative – it tidies up the mess of the world and shapes publics through their participation (Law, 2004). Our social science apparatus for eliciting public opinions and enacting public science sits somewhere in the middle of Chilvers and Kearns' (2015) *in vivo*–*in vitro* spectrum. We had assembled a public, in a similar fashion to the laboratory conditions of an *in vitro* focus group, but the open-ended and recursive design of our group experiments let participants run “wild,” taking the tools of metagenomics into their homes and putting them to work in *in vivo* settings. At times our participants “misbehaved” (after Michael, 2012) – going off script with the experiment or its interpretation. But the project was flexible and reflexive (cf. Krzywoszynska et al., 2018) enough to keep them on board and, in so doing, to shed light on new dimensions of domestic hygiene and vernacular microbiology (see below). In shuttling between the community centre and the homes of our participants, the methodology created novel epistemic conditions for social science enquiry.

Third, perhaps the most striking contribution of these novel epistemic conditions stemmed from the way in which they shifted the microbiome from a closed scientific object to a public “epistemic thing” (Rheinberger, 1997). We were able to make the microbiome a subject of enquiry capable of generating surprises and of making new knowledge possible. In a similar way to Whatmore and Landstrom's (2011) flood-risk model, the recursive, pluralistic and democratic nature of knowledge production in our workflow helped to “slow down” and “open up” our own and our participants' reasoning processes. We found the potential of surprises was best expressed in our management of the group meetings as a collective learning cycle. Through repeated experiments, analysis and discussion, we arrived at a shared language for grappling with the science and technology of metagenomics and the microbial realities it brought into being, and for attuning to when microbiome science confounded established thinking about hygiene. This potential was perhaps best illustrated in the

experiment on cleaning products, in which participants swabbed their worktops before and after application, alongside their cleaning cloths. These cloths emerged as biodiversity hotspots, teeming with microbial life. This was not expected, and caused surprise, excitement and consternation in equal measure. It prompted rich discussions with our participants and the FSA scientist (who had joined us for this group meeting) about kitchen ecologies – cloths as ecological restoration devices – as well as swift behaviour change among some participants (hot washing or shifting to paper towels).

According to the typology offered by Callon et al. (2009) for evaluating this type of “hybrid forum” between scientists and publics, our methodology went a long way towards facilitating “collaborative research,” involving the engagement by our public in the “formulation of problems,” “the extension and organisation of the research collective” and “the application of laboratory results in the real world.” We were less successful in reorganising our political collective towards a “dialogical model” for managing domestic hygiene and how it is governed, but this was never our aim. In contrast to Whatmore et al.’s apprenticeship model, and other modes of public engagement that focus on designing solutions or making decisions, there was no consensus position or practical intervention that emerged from our collective learning that the group felt necessary to take forward. We did not set out to achieve this, but the mode of microbiome research that was generated through this mode of engagement points towards where such collectives may emerge in the future, for example around hot microbiopolitical topics like antibiotic stewardship, faecal transplant, food safety or soil health (Granjou & Phillips, 2018; Spackman, 2018).

## 5.2 | Participatory microbiome science as a tool for social science research

Our participatory sequencing methodology proved to be a powerful tool for social science research on domestic hygiene. Thinking with the microbial ecologies revealed by our participatory experiments moved well beyond the interview, observational and focus group methodologies that predominate in research in this area (Wills et al., 2013). It gave participants training, a clear motivation to think with microbes and microbial ecologies, and a stake in the outcome of their experiments. The longitudinal and recursive design of the sequential group experiments enabled us to follow changes over time. We could return to our participants to explore emerging understandings and to discuss further questions. It thus worked effectively with the mode of spiral, collective learning that underpinned our apprenticeship model. The novel, generative potential of this approach was most clear when participants were surprised that the results of an experiment did not conform to their expectations. From a social science perspective, these surprises, the confusion they engendered and the ways in which they were discussed and rationalised within the group were particularly informative.

We report on what we learnt in more detail elsewhere (Greenhough et al., 2018). Here we will briefly reflect on how participating in this project affected our participants’ ideas about antibiotic and probiotic approaches to domestic hygiene. Many of us and our participants were taken by the “microbial sublime” that drives popular representation of the microbiome: the idea that humans are radically pre-dated, outnumbered and dependent on our microbial symbionts. Our participants remained curious and stayed the course of the project, in spite of its challenges and frustrations. Thinking hygiene with microbial ecologies in a group setting over time put some of our (sometimes trenchant) ideas about hygiene at risk and forced us as a group to think about cleaning differently. By the end of the process, participants agreed that being clean was not indexed to the absence of microbes but related more to the absence of visible dirt and/or noxious odours. They reported a broad tolerance for commensal bacteria – the ones that are there and do us no harm. This tolerance grew as their experiments revealed the limited effects of their cleaning interventions on the diversity and abundance of the kitchen microbiome, and thus the impossibility of sterility and microbial eradication. Many were drawn to the idea emerging in the scientific literature of their domestic animals as probiotic additions to their household: this was the most popular focus on the final individual experiments. But at the same time, they remained sceptical of the idea that kitchens could be managed for beneficial bacteria. While they were happy to accept the logic of introducing probiotic strains of microbes into the gut, there was limited enthusiasm for new thinking that suggests that domestic hygiene practices might be recalibrated to nurture stable functional microbial ecologies to limit the abundance and spread of pathogenic bacteria. They were wary of using the commercially available probiotic spray we offered for the cleaning products experiment that claims to seed kitchen surfaces with bacteria that eat biofilms before establishing a benign ecology.

Our experience in these group meetings made clear the need for new popular imaginaries for understanding the ubiquity and diversity of the microbiome and its implications for everyday life (Nerlich & Hellsten, 2009). Our project demonstrated how difficult it is to transcend a century of public health messaging around “germs,” and societal understandings of “species” as identifiable and knowable categories. We experimented with different narratives and metaphors as we presented the results of the experiments. We encouraged participants to compare their kitchen surfaces to familiar habitats: the desert (cupboard top), the rainforest (the bin), swamp (plug hole), ice cap (fridge/freezer), oceanic thermal vents (kettle), the arable

field (worktop), etc. We also encouraged them to compare domestic cleaning to gardening, to explore questions of temporal change, the value of diversity and the potential of desired stable ecologies (the lawn) to keep undesired species (weeds) at bay. We floated the idea of microbial extinction and conservation. In the end of project interviews, we found several of our participants drew unprompted on these metaphors when they explained how they now conceived of the microbes in their kitchen. But there is more work to be done here by social scientists to understand vernacular models of natural history and how they might be leveraged for public participation with microbiome science.

The social, deliberative character dimension of this project also helped reveal the complex ways in which domestic hygiene is culturally coded, and how microbes are made moral (Tomes, 1999). Knowing that the project was a collaboration with the FSA, participants were initially concerned that we were going to rank how clean their houses were. Some acknowledged that they cleaned before we came for interview. Here cleanliness – marked by the visible absence of dirt and smells – was a moral virtue, and testament to good housekeeping (Martens & Scott, 2005). For others, this modern or antiseptic model was associated with their parents, raised in post-war Europe with the lingering threat of infectious disease and food contamination, and subject to the wholehearted embrace of sanitary chemicals. Living in the antibiotic age of the late 20th and early 21st century, they were agnostic about the moral virtues of sterility and reacted against their parents' advice. Their encounters with the microbiome fuelled a more *laissez-faire* and ecological identity that pushed back against the proliferation of antibacterial chemicals and the established forms of public and private knowledge that promote their application (cf. Paxson, 2008, 2014). They referred to biodiversity loss, pollution and the rise of autoimmune disease, and articulated wider millennial anxieties about a global ecological crisis (cf. Tauber, 2017 on the rise of eco-immunology). This project just scratched the surface of the complex ways in which these popular ideas of hygiene interface with anxieties about biome depletion, and more research is required.

## 6 | THE FUTURE OF PARTICIPATORY RESEARCH ON THE MICROBIOME

In spite of the efforts of a range of citizen-science and crowd-sourced initiatives, metagenomics currently remains an esoteric and centralised practice. The microbiome is still largely a scientific object and stands as the black-boxed outcome of the secluded processes of laboratory research. Nonetheless, knowledge about the microbiome and its management increasingly overflows the laboratory and interfaces with public anxieties about hygiene. As we write this conclusion, the media is reporting a new study that links the incidence of childhood leukaemia to the absence of childhood infection (Greaves, 2018), alongside vague instructions as to how worried parents might secure the right type of infections: “ultra clean homes” are pathologised (Knapton, 2018). It is clear that microbial literacy is becoming a necessary part of technical democracy. This project contributes to the project of making the microbiome public that this will require.

The methodology we have developed is expensive, cumbersome and time consuming. But we are optimistic that some of the technical challenges we have identified will be overcome in the near future. The rise of portable sequencing, including the simplification of the procedures for sample preparation, coupled with the growing sophistication and accessibility of microbiome visualisation software, will accelerate the movement of metagenomics into society. The key question, as ever with technologies explicitly bent on being “disruptive,” relates to the nature of their social impact. A consumer sequencer could significantly reconfigure how various stakeholders and publics understand themselves, their interactions with others and a wide range of environmental processes. It will bring new forms of microbial citizenship into existence. Such a device would no doubt fuel the current growth in quantified microbial selves (Lupton, 2016) and experiments in personalised DIY biology. It would raise novel and familiar issues regarding the prospecting, ownership and security of genetic information (Parry & Greenhough, 2017) and the potential use of the microbiome for forensic and diagnostic purposes.

The research presented in this paper suggests that the future direction and success of such technological developments must first be premised on a better understanding of their potential publics. Making a public sequencer will require more accessible platforms for data visualisation, the cultivation of new microbiological ontologies and knowledges among affected publics, and the existence of robust and standardised data sets that will allow users to undertake meaningful analysis of their gathered data. Without them, these technologies may create anxieties and possible harm, given the findings of our research that publics struggle to make sense of what the data means, or what to do about it. Second, whether or not these technologies lead to the genuine “democratisation of sequencing” (Check Hayden, 2015) will relate in large part to the political and economic relations that surround the commercialisation of both the device itself and the data that it generates.

The methodology developed in this paper, and the growing body of constructively critical work on the microbiome, metagenomics and other public science interventions, establishes an agenda for tailoring the democratisation of sequencing. This research helps those deploying metagenomic tools, and the data they produce, for the wider investigation of

social practices, and for the mobilisation and redirection of new and existing publics. We see ample opportunity for geographers and other social scientists to engage with metagenomics and with microbiologists. These collaborations would develop research projects that aim to both nurture the transformative political potential of this new technology and to harness its ability to generate novel insights into established social norms and practices. We see obvious future applications for participatory research on topics that span and link the current spaces of microbiome science. New opportunities could encompass topics as diverse as gut dysbiosis, water and soil quality, agricultural biosecurity or the communal relationships mediated by microbes in public and institutional settings (transport, schools, offices or the circulation of money, etc.). Making the microbiome public promises timely and democratic tools for addressing fundamental questions of human and environmental health.

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## DATA ACCESSIBILITY

Data from this project are publicly accessible. Transcripts of the interviews have been deposited in the UK Data Archive <https://doi.org/10.5255/UKDA-SN-853055>. Biological data will be deposited in the NCBI Sequence Read Archive.

## ENDNOTES

- <sup>1</sup> The design of this methodology was informed by a review of existing methods for making the microbiome public, including a series of interviews conducted with key stakeholders in microbiome research in 2016–2017.
- <sup>2</sup> For a short visual introduction to the project, see this film: <https://youtu.be/rdmejCxWblc>.
- <sup>3</sup> The questionnaire gathered background information on the household, its members and their interests. It also helped screen for respondents with expert microbiological knowledge and/or a medical condition that might affect their participation in the project. We had intended to exclude anyone with such a stake in the microbiome, but this did not prove to be necessary.
- <sup>4</sup> We are especially grateful for the advice we received from Rob Dunn, Jeff Coil, Anne Madden and Holly Menniger.
- <sup>5</sup> See [www.giantmicrobes.com](http://www.giantmicrobes.com).

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